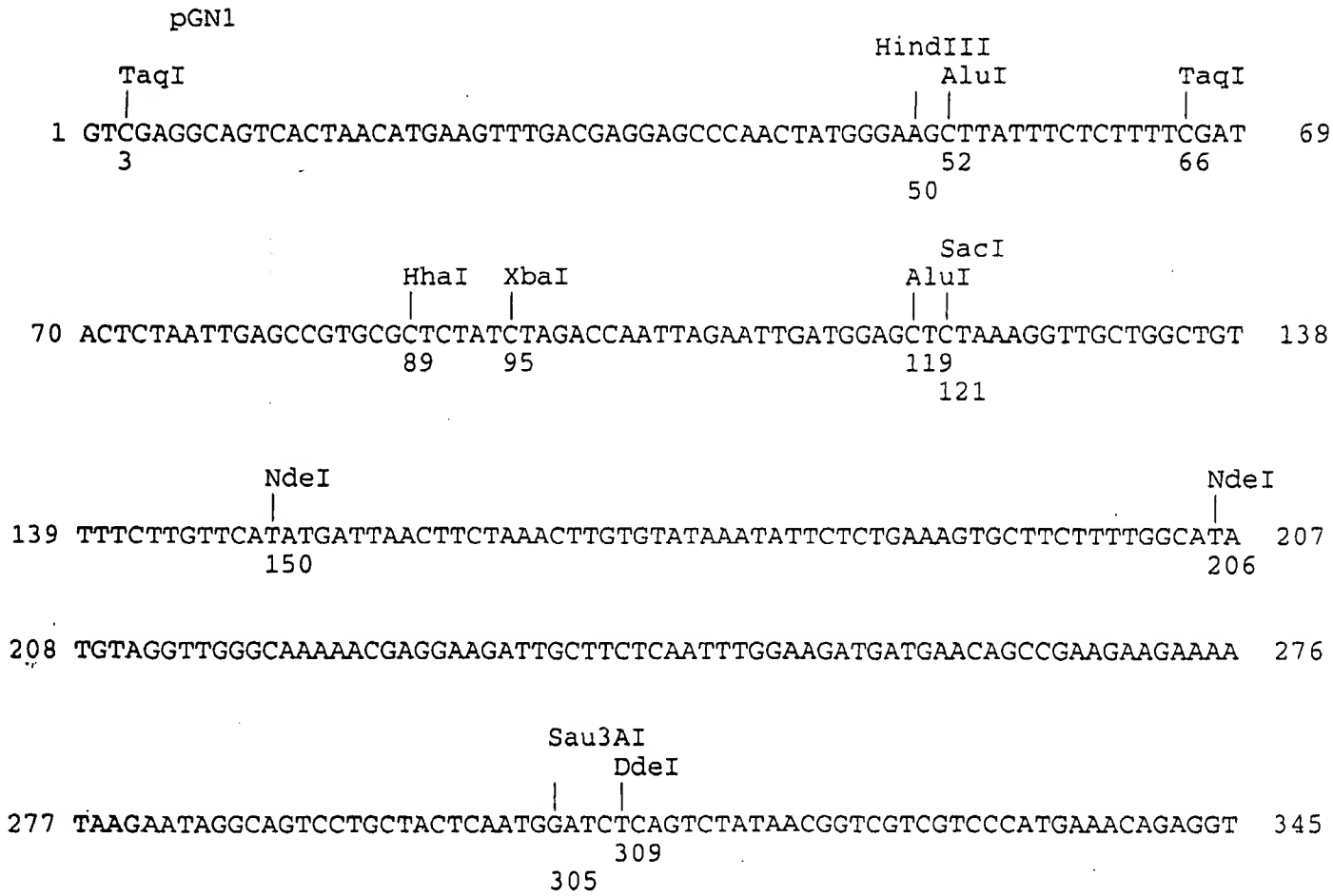

FIG. 1A

```
EcoRV
                                                                 |
346 AACACATTTTTGCATATACACTTTGATAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA  414
                                                                 408

                         NaeI
                        MspI
                        HpaII
                 AluI  HhaI                                 HaeIII      AluI
                  |    |||                                   |           |
415 CAATGTTGGAGAGACAANGCTGCGCJRRCATATACAGAAGGGAAATGAAGATGGCCTTTTGATTAGCTG  483
                  434  439                                   469         481
                        440
                        440
                         441

              AluI                                     HinfI
               |                                        |
484 TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA  552
               498                                      535

           MspI
           HpaII                                        HinfI
            |                                            |
553 TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATCTGATTTGT  621
            564                                          606
            564

       DdeI
        |
622 AGTAAACTAAGAAGAACTTACCTTATGATTTCCCCGCAGGACTGGATTATGGAACAATGGGAAAAGAAC  690
        629
```

FIG. 1B

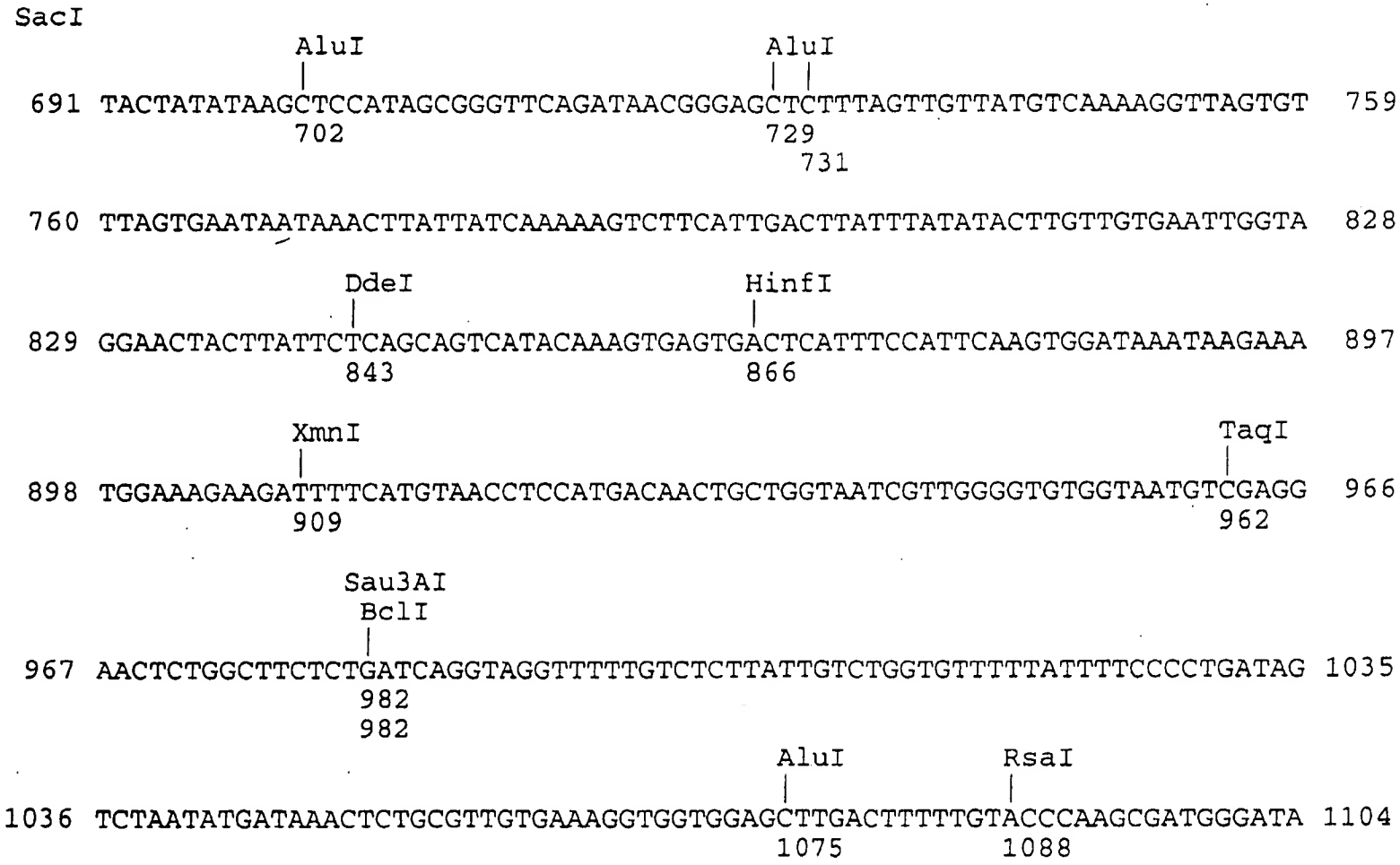

FIG. 1C

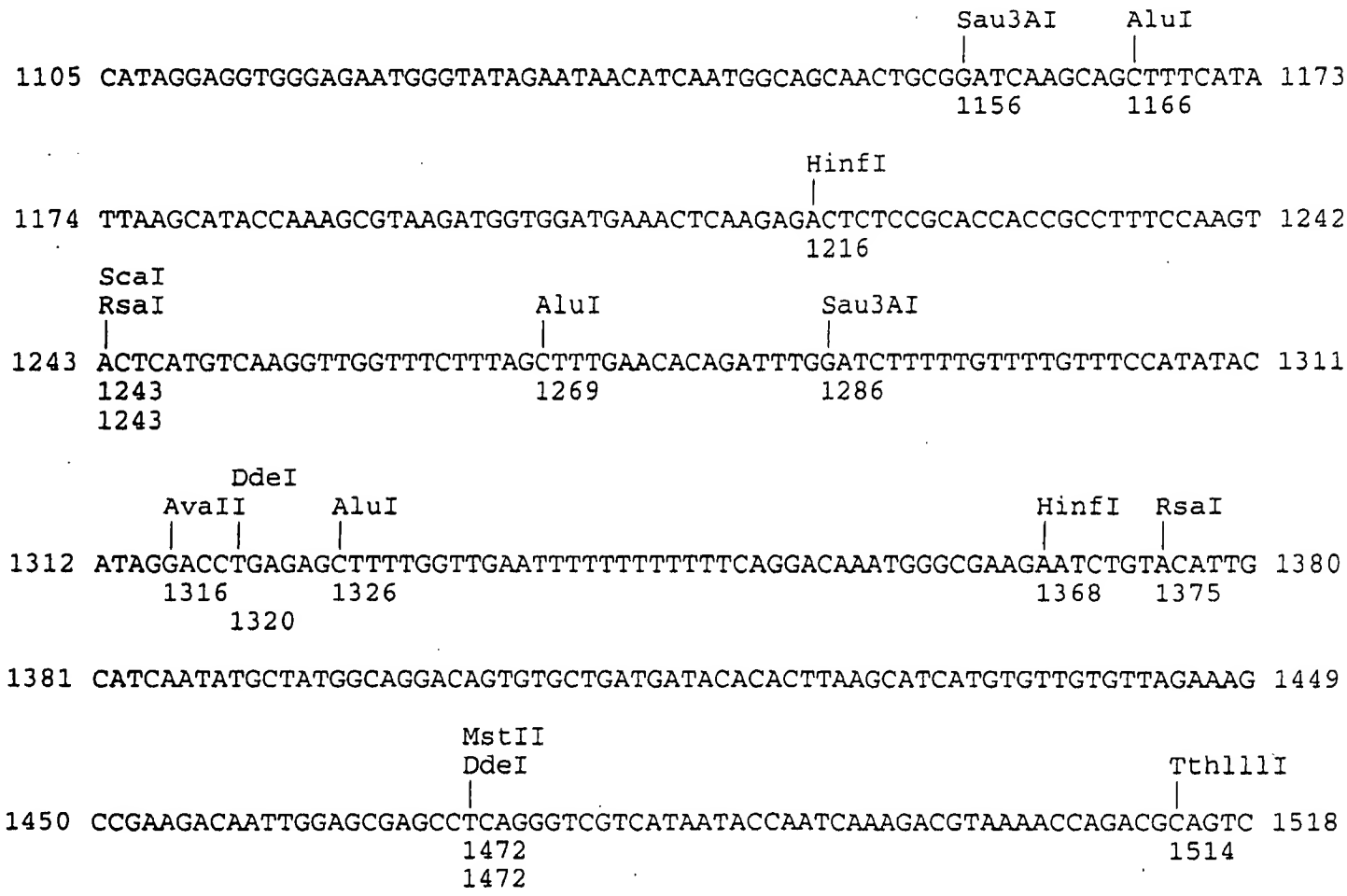

FIG. 1D

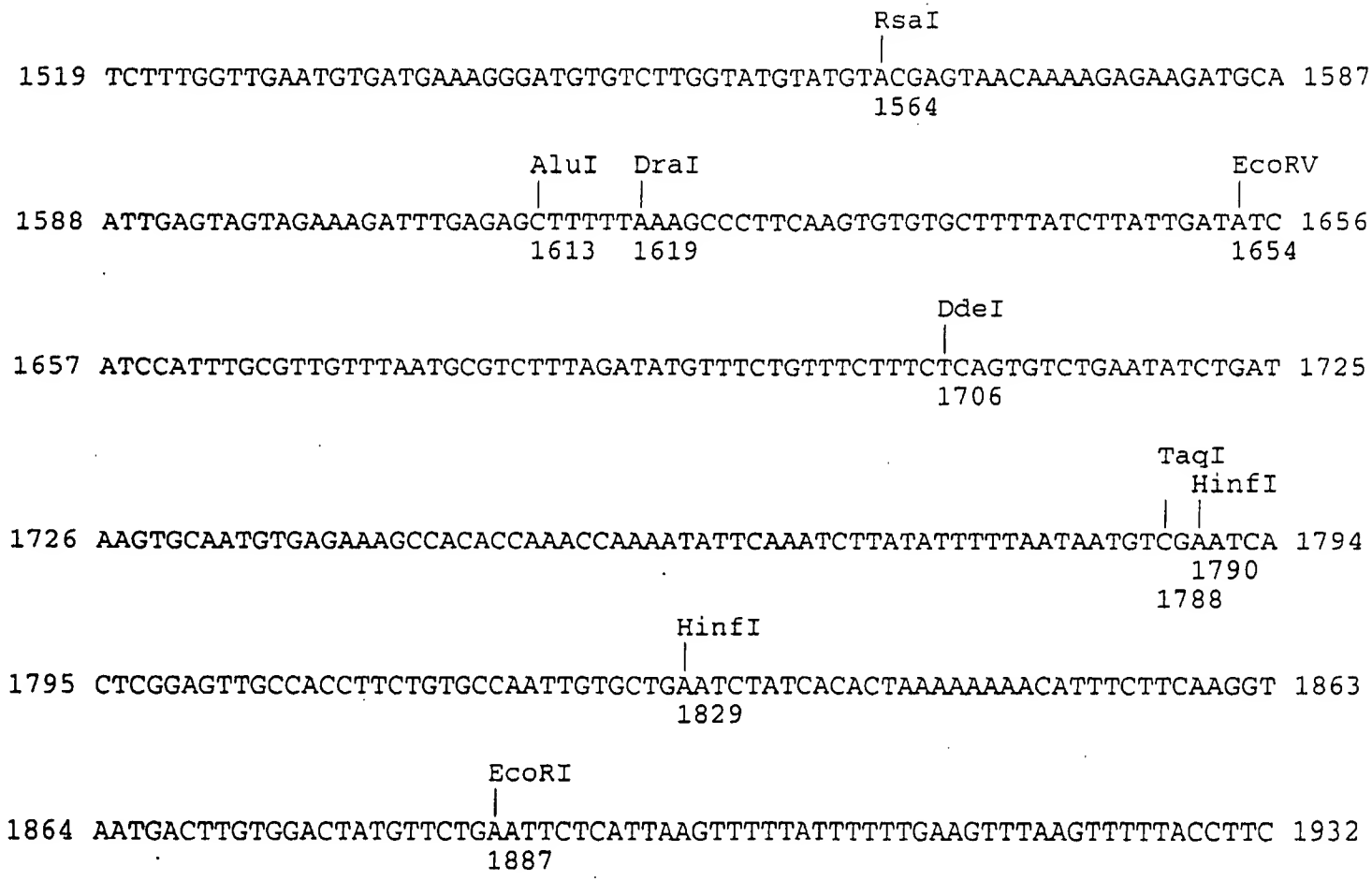

FIG. 1E

```
                                                     BstNI        AluI                        SphI
                                                     |            |                           |
1933 TTTTTTGAAAAATATCGTTCATAAGATGTCACGCCAGGACATGAGCTACACATCACATATTAGCATGCA 2001
                                                     1968         1978                        2000

                                                            AluI                          NdeI
                                                            |                             |
2002 GATGCGGACGATTTGTCACTCACTTCAAACACCTAAAAGAGCTTCTCTCTCACAGCACACACACATATG 2070
                                                            2043                          2067

        SphI
     NsiI          Sau3AI
     | |           |
2071 CATGCAATATTTACACGTGATCGCCATGCAAATCTCCATTCTCACCTATAAATTAGAGGCTCGGCTTCA 2139
     2073          2089
       2075

                                                                              AluI
                                                                              |
2140 CTTTTTACTCAAACCAAAACTCATCACTACAAAACATACACAAATGGCGAACAAGCTCTTC 2200
                                                   Met                        2195
```

FIG. 1F

```
Lambda CGNI-2

NCG-I86 Linear           Length = 4325

 XhoI
  TaqI                                                               HindIII
 AvaI                                                                  AluI         TaqI
 ||                                                                  | |             |
CTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT    69
 2                                                                     52            66
  3                                                                  50

                                                                      SacI
                  HhaI  XbaI                                         AluI
                   |     |                                           | |
ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT   138
                   89    95                                          119
                                                                       121

           NdeI                                                                NdeI
           |                                                                   |
TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA   207
           150                                                                 206

TGTAGGTTGGGCAAAAACGAGGAAGATTGCTTCTCAATTTGGAAGAGGATGAACAGCCGAAGAAGAAAA   276

                                Sau3AI
                                    DdeI
                                |   |
TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTCGTCCCATGAAACAGAGGT   345
                                    309
                                305
                                                                  EcoRV
                                                                     |
AAAACATTTTTTGCATATACACTTTGAAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA   414
                                                                  408
```

FIGURE 2A

```
                             HincII
                               HhaI
                              HaeIII
                              DdeI
                             BstEII
                              BalI                                HaeIII        AluI
                              |||                                   |             |
CAATGTCGGAGAGACAA3GGCTGMNCANCATATACAAAAGGGAAATGAAGATGGCCTTTTGATTAGCTG    483
                              439                                  469           481
                             438
                               440

               AluI                                            HinfI
                |                                                |
TGTAGCATCAGCAGCTAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA    552
               498                                              535

            MspI
            HpaII                                                 HinfI
             |                                                     |
TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATTTGATTTGT    621
            564                                                   606
            564

       DdeI
        |
AGTAAACTAAGAAGAACTTACCTTATGTTTTCCCCGCAGGACTGGATTATGGAACAATGGAAAAGAAC    690

       629
                                                 SacI
            AluI        AluI                    AluI
             |            |                      | |
TACTATATAAGCTCCATAGCTGGTTCAGATAACGGGAGCTCTTTAGTTGTTATGTCAAAAGGTTAGTGT    759
            702          710                   729
                                                 731
```

FIGURE 2B

```
TTAGTGAATAATAAACTTATACCACAAAGTCTTCATTGACTTATTTATATACTTGTTGTGAATTGCTAG   828

          DdeI                           HinfI
          |                              |
GAACTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT   897
           842                           865

        XmnI                                                       TaqI
        |                                                          |
GGAAAGAAGATTTTCATGTAACCTCCATGACAACTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGGA   966
        908                                                        961

            Sau3AI
            BclI
            |
ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTTTTTATTTTCCCCTGATAGT  1035
            981

                                       AluI         RsaI
                                       |            |
CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTTGTACCCAAGCGATGGGATAC  1104
                                       1074         1087

                                                         Sau3AI    AluI
                                                         |         |
ATAGGAGGTGGGAGAATGGGTATAGAATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTCATAT  1173
                                                         1155      1165

                                                                   ScaI
                                          HinfI                    RsaI
                                          |                        |
TAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCACCGCCTTTCCAAGTA  1242
                                          1215                     1242
```

FIGURE 2C

FIGURE 2D

```
                                   HinfI
                                   |
ACCAAAATATTCAAATCTTATTTTTAATAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATTG  1794
                                   1761

   HinfI                                                         EcoRI
   |                                                              |
TGCTGAATCTATCACACTAGAAAAAAACATTTCTTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC  1863
   1800                                                          1859

TCATTAAGTTTTTATTTTCTGAAGTTTAAGTTTTTACCTTCTGTTTTGAAATATATCGTTCATAAGATG  1932

                                     SphI
    BstNI     AluI                    Sau3AI
    |         |                     | |
TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTTGTCACTCACTTCAAA  2001
    1940      1950                    1973
                                     1971

                                          SphI
  DdeI  AluI            HhaI    NdeI   NslI             Sau3AI
  |     |               |       |      | |              |
CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCAATATTTACACGTGATCGCCATGCAA  2070
  2006  20I2            2028    2036   2042             2058
                                        2044

ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAACCAAAACTCATCACTACA  2139

                        AluI
                        |
GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTCGGCAACTCTCGCCTTGTTCTTCCTTCTCACC  2208
            MetAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPhePheLeuLeuThr

                             2164
```

FIGURE 2E

```
                 TaqI                   NaeI
                    SalI                    MspI
                   HindII                   HpaII
     AccI          AccI                    HaeIII
     |             |||                    || |
AATGCCTCCGTCTACAGGACGGTTGTGGAAGTCGACGAAGATGATGCCACAAATCCAGCCGGCCCATTT  2277
AsnAlaSerValTyrArgThrValValGluValAspGluAspAspAlaThrAsnProAlaGlyProPhe
        2220                 2241                        2271
                           2239                       2268
                            2240                       2269

                                                HindIII
 HinfI                                       AluI
  |                                           | |
AGGATTCCAAAATGTAGGAAGGAGTTTCAGCAAGCACAACACCTGAAAGCTTGCCAACAATGGCTCCAC  2346
ArgIleProLysCysArgLysGluPheGlnGlnAlaGlnHisLeuLysAlaCysGlnGlnTrpLeuHis
    2281                                     2327
                                                2325

         MspI              AvaII
              HpaII    AvaII  AluI       TaqI
         |       |      |  |     |
AAGCAGGCAATGCAGTCCGGTAGTGGTCCAAGCTGGACCCTCGATGGTGAGTTTGATTTTGAAGACGAC  2415
LysGlnAlaMetGlnSerGlySerGlyProSerTrpThrLeuAspGlyGluPheAspPheGluAspAsp
                    2364    2372   2379    2388
                                      2382

                 HaeIII                                         SacI
                   ApaI      HaeIII                           AluI
                 |  |       |                               |  |
GTGGAGAACCAACAACAGGGCCCGCAGCAGAGGCCACCGCTGCTCCAGCAGTGCTGCAACGAGCTCCAC  2484
ValGluAsnGlnGlnGlnGlyProGlnGlnArgProProLeuLeuGlnGlnCysCysAsnGluLeuHis
                   2438       2449                            2479
                 2436                                           2481
```

FIGURE 2F

FIGURE 2G

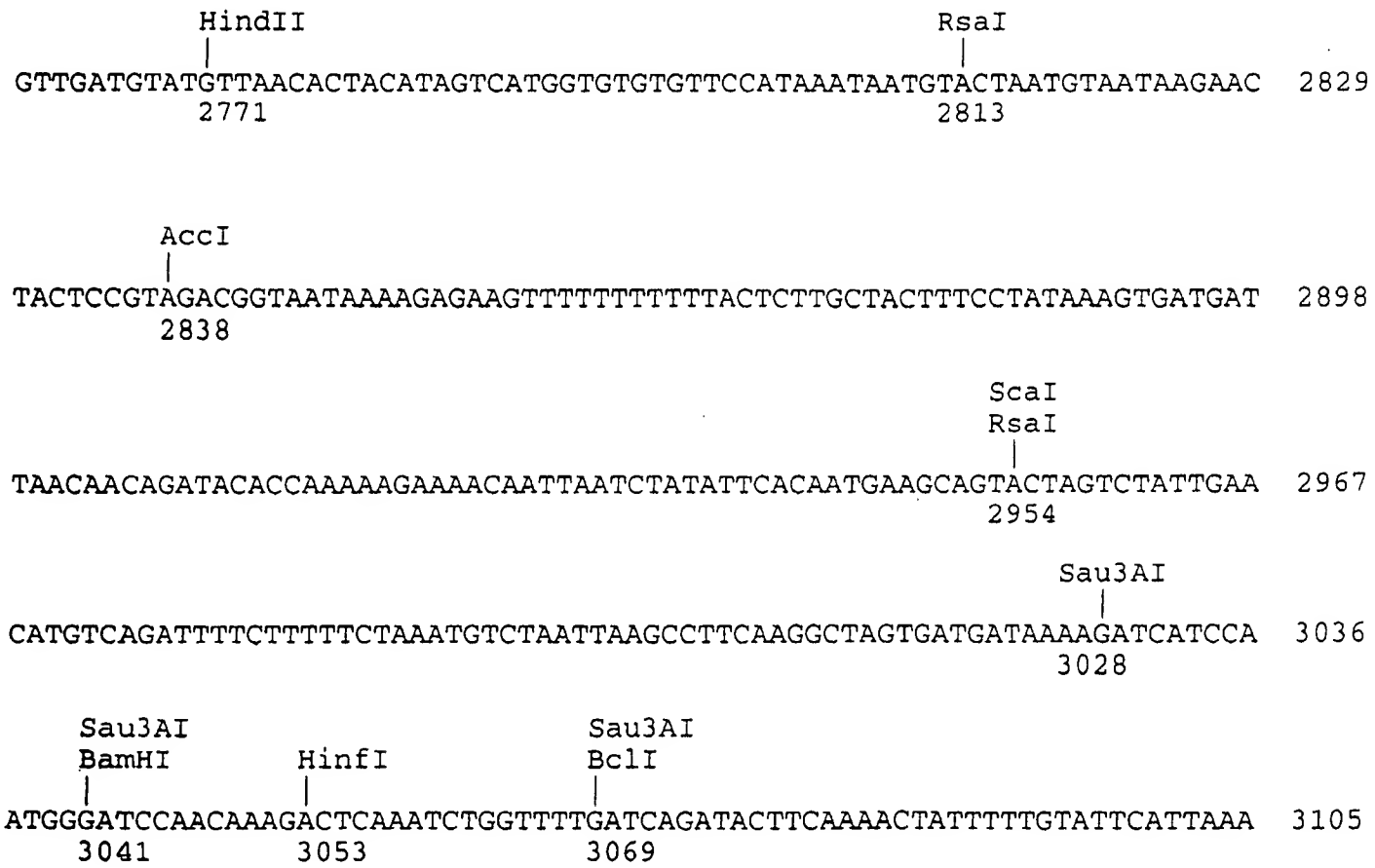

FIGURE 2H

```
                                 HinfI
                                   |
TTATGCAAGTGTTCTTTTATTTGGTGAAGACTCTTTAGAAGCAAAGAACGACAAGCAGTAATAAAAAAA  3174
                                 3135

ACAAAGTTCAGTTTTAAGATTTGTTATTGACTTATTGTCATTTGAAAAATATAGTATGATATTAATATA  3243

GTTTTATTTATATAATGCTTGTCTATTCAAGATTTGAGAACATTAATATGATACTGTCCACATATCCAA  3312

                                NdeI
                                  |
TATATTAAGTTTCATTTCTGTTCAAACATATGATAAGATGGTCAAATGATTATGAGTTTTGTTATTTAC  3381
                                3341

                             TaqI                   Sau3AI
                           AluI                   RsaI
                           |  |                    |  |
CTGAAGAAAAGATAAGTGAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTTCTTGGCTAAAAGCGA  3450
                           3402                    3421
                              3405                    3425

ATATGACATCACCTAGAGAAAGCCGATAATAGTAAACTCTGTTCTTGGTTTTTGGTTTAATCAAACCGA  3519

                                                                MspI
  MspI   DdeI                                                   HpalI
  HpalI AluI                                    NdeI       HinfI
  |     ||                                       |          |    |
ACCGGTAGCTGAGTGTCAAGTCAGCAAACATCGCAAACCATATGTCAATTCGTTAGATTCCCGGTTTAA  3588
  3522  3528                                    3560       3576
         3529                                                   3581
```

FIGURE 2I

```
          MspI
          HpalI
          |
GTTGTAAACCGGTATTTCATTTGGTGAAAACCCTAGAAGCCAGCCANCCTTTTTAATCTAATTTTTGCA  3657
          3598

                                                              HinfI
                                                               HincII
                                                    DdeI          BstNI
                                                    |          || |
AACGAGAAGTCACCACACCTCTCCACTAAAACCCTGAACCTTACTGAGAGAAGCAGAGNCANNAAAGAA  3726
                                                    3702          3718
                                                               3715
                                                              3714

CAAATAAAACCCGAAGATGAGACCACCACGTGCGGCGGGACGTTCAGGGGACGGGGAGGAAGAGAATGR  3795

     AvaII                                                            AvaII
        AluI                                                            |
     |  |
CGGCGG5MNTTTGGTGGCGGCGGCGGACGTTTTGGTGGCGGCGGTGGACGTTTTGGTGGCGGCGGTGGA  3864
        3804                                                         3863
     3801

               EcoRV       AvaII                                 DdeI
               |           |                                     |
CCTTTGGTGGTGGATATCGTGACGAAGGACCTCCCAGTGAAGTCATTGGTTCGTTTACTCTTTTCTTAG  3933

               3880        3892                                 3930
```

FIGURE 2J

FIGURE 2K

4325

TaqI
SalI
PstI
HincII
HindIII
Sau3AI AluI
AccI EcoRI

TGGGAAAGTTGATGAGATCCAAGCTTGGGCTGCAGGTCGACGAATTC

4294 4302 4316 4321
4300 4314
4313
4315

FIGURE 2L

Brassica campestris ACP Genomic Sequence

```
                                                         DdeI
              AccI                                      AluI AluI
              |                                         ||   |
  1 AAGAGTATGTCTACTACTACTACTCTATAATCAAGTTTCAAGAAGCTGAGCTTGGCTCTCACTTTATAT   69
              11                                        46   51
                                                         47

 70 GTTTGATGTTGTTGTGCAGGTATGGTAAATCATGGAAAGAGATAAAGAATGCAAACCCTGAAGTATTGG  138

             DdeI
             |
139 CAGAGAGGACTGAGGTGAGAGAGCATGTCACTTTTGTGTTACTCATCTGAATTATCTTATATGCGAATT  207
             149

            RsaI
            |
208 GTAAGTGGTACTAAAAGGTTTGTAACTTTTGGTAGGTGGATTTGAAGGATAAATGGAGGAACTTGCTTC  276

                                     HindIII                       PvuII
                                      AluI                         AluI
                                     | |                           |
277 GGTAGCGGTAACAAGTTTTATATTGCTATGAAGCTTTTTTGCCTGCGTGACGTATCAGCAGCTGTGGAG  345
                                      310                          338
                                     308                           338
```

FIGURE 3A

```
                    MspI
                    HpaII
                    HaeIII
                    ||
346 AAGATGGTATTAGAAAGGGTCTTTTCACATTTTGTTGTGACAAATATTAATTCGGCCGGTATGGTTT  414
                                                    403
                                                    404
                                                    404

415 GGTTAAGACTTGTTGAGAGACGTGTGGGGTTTTTTGATGTATAATTAGTCTGTGTTTAGAACGAAACAA  483

                                                          Tth111I
                                                          |
484 GACTTGTTGNGTATGCTTTTTTTTAACTTGAGGGGGTTTGTTGTTAGTTAGGAACTTGACTTTGTCT  552
                                                                547

                                ScaI
                                RsaI
                                |
553 CTTTCTCTCAAGATCTGATTGGTAAGGTCTGGGTGGTAGTACTGTTTGGTTTAATTTGTTTTTGACTATT  621
                    564
                    564
                    593
                    593

                                                    HpaII
                                                    DraI MspI DdeI
                                                    |    |    |
                    Sau3AI
                    BglII
                    |
                    HinfI     HaeIII     DraI
                    |         |          |
622 GAGTCACTGTGGCCCATTGACTTTAAATTAGGCTGGTATATTTTTTGGTTTTAAAACCGGTCTGAGATAG  690
    623       634        646                673  678  683
                                                678
```

FIGURE 3B

```
            TaqI
              HinfI         DraI
            | |             |
691 TGCAATTTCGATTCAGTCAATTTTAAATTCTTCAAGGTAATGGGCTGAATACTTGTATAGTTTTAAGAC 759
              701           715
            699

            StuI                                             HindIII
            HaeIII    HaeIII                                   AluI
            |         |                                      | |
760 TTAACAGGCCTTAAAAGGCCCATGTTATCATAAAACGTCATTGTTTAGAGTGCACCAAGCTTATAAAAT 828
            768       778                                      819
            768                                              817

             StuI
             HaeIII             StuI
          BstNI                 HaeIII                       HaeIII
          |  |                  |                            |
829 GTAGCCAGGCCTTAAAAGACTTAACAGGCCTTAAAAGACTTAACATTCCTTAAAAGGCCCATGTTATCA 897
          835                   857                          886
             838                857
             838

                                                StuI
                                                HaeIII             StuI
                                 AluI        BstNI                 HaeIII
                                 |           |  |                  |
898 TAAAACGTCATCGTTTTGAGTGCACCAAGCTAAATGTAGCCAGGCCTTAAAAGACTTAACAGGCCTTAA 966
                                 927         939                   961
                                                942                961
                                                942
```

FIGURE 3C

```
                                                     HindIII
         HaeIII                                        AluI                        AluI AvaI
          |                                          | |                            |    |
967 AAGGCCCATGTTATCATAAAACGCCGTCGTTTTGAGTGCACCAAGCTTATAAATGTAGCCAGCTACCTC 1035
         971                                           1012                        1029 1034
                                                     1010

                                                    XhoI
                                                     TaqI  Sau3AI
                        RsaI                        AvaI   BglII   AvaI       TaqI
                         |                          ||      |       |          |
1036 GGGACATCACGCTCTTTGTACACTCCGCCATCTCTCTCTCTCTCGAGCAGATCTCTCTCGGGAATATCG 1104
                        1055                        1078   1085    1093       1103
                                                     1079  1085
                                                    1078

           Tth111I
               TaqI
              SalI
             HincII
               AccI
           |  |||
1105 ACAATGTCGACCACTTTCTGCTCTTCCGTCTCCATGCAAGCCACTTCTCTGGTAATCTCATCTCCTTCT 1173
           METSerThrThrPheCysSerSerValSerMETGlnAlaThrSerLeu
               1112
             1110
              1111
               1112
           1108
```

FIGURE 3D

FIGURE 3E

```
                                                             HhaI                DdeI
                                                               |                   |
1519 TCCTTCAACCTCCGCCGTTCAATCCCCACTCGTTTCTCAATCTCCTGCGCGGTATGTTCTCATTCTCAG 1587
     SerPheAsnLeuArgArgSerIleProThrArgPheSerIleSerCysAla
                                                               1568                1584

                TaqI
                     AluI                RsaI                                HaeIII
                |    |                   |                                     |
1588 CATTTATTTCGAGCTTGCTTGTCATGGTACTCTCTCTAATTGTCTATTTGGTTTATTAGGCCAAACCAG 1656
                                                                         AlaLysProG
                     1601                1616                              1648
                1597

                         DdeI                     AluI
                           |                        |
1657 AGACGGTTGAGAAAGTGTCTAAGATAGTTAAGAAGCAGCTATCACTCAAAGACGACCAAAAGGTCGTTG 1725
     luThrValGluLysValSerLysIleValLysLysGlnLeuSerLeuLysAspAspGlnLysValValA
                           1676                     1695

                        Sau3AI            HinfI    TaqI
                          |                 |        |
1726 CGGAGACCAAGTTTGCTGATCTTGGAGCAGATTCTCTCGACACTGTAAGTCATCAATCATTCTCTTATG 1794
     laGluThrLysPheAlaAspLeuGlyAlaAspSerLeuAspThr
                          1743              1756     1763

                                                         DdeI                 SphI
                                                           |                    |
1795 TGAATAAAGAGAACTTGAAGAGTTTGTTTTTAACATATTAACTGAGTGTTTTGCATGCAGGTTGAGATA 1863
                                                                          ValGluIle
                                                           1837                 1852
```

FIGURE 3F

```
                                        TaqI                                  DdeI
                                       EcoRV                                 AluI
                                       |  |                                  ||
1864 GTGATGGGTTTAGAGGAAGAGTTTGATATCGAAATGGCTGAAGAGAAAGCTCAGAAGATTGCTACTGTG 1932
     ValMetGlyLeuGluGluGluPheAspIleGluMetAlaGluGluLysAlaGlnLysIleAlaThrVal
                                       1891                                  1913
                                          1893                                1914

                                          SacI
           AluI                        AluI
           |                           |  |
1933 GAGGAAGCTGCTGAACTCATTGAAGAGCTCGTTCAACTTAAGAAGTAATTTTAGTATTAAGAGCAGCCA 2001
     GluGluAlaAlaGluLeuIleGluGluLeuValGlnLeuLysLys
           1940                        1960
                                          1962

                                                                        HinfI
                                                                        |
2002 AGGCTTTGTTGGGTTTGTTGTTTTCATAATCTTCCTGTCATTTTCTTTTTCTTTAATGTGTCAAGCGAC 2070
                                                                        2069

                                                                     TaqI
                                                                    SalI
                                             Sau3AI                HincII
              DraI                      NcoI                          AccI
              |                         |     |                    |||
2071 TCTGTTGGTTTAAAGTAGTATCTGTTTGCCATGGATCTCTCTCTATTTGTCGACTGAAAACTTTTGGTT 2139
              2082                      2100                          2121
                                              2104                 2119
                                                                    2120
                                                                    2121

          HindIII
              AluI
          |  |
2140 TACACATGAAAGCTT 2154
                 2152
              2150
```

FIGURE 3G

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Brassica Campestris Seed Specific cDNA-EA9

```
                                        Sau3AI
                                          |
  1 TTCAACTTTTCTAAACCAAATGGCTTTAACACAGATCCAAATCTTTCTCATTGTCTCTCTAGTCTCATC   69
                        METAlaLeuThrGlnIleGlnIlePheLeuIleValSerLeuValSerSe
                                        34

                 TaqI
                  Sau3AI
                 ClaI                          TaqI
                  ||                            |
 70 ATTCAGTTTATCGATCACTCTTTCTCGTCCATTACTCGATGAAGTCGCCATGCAAAAGAGACATGCCGA  138
    rPheSerLeuSerIleThrLeuSerArgProLeuLeuAspGluValAlaMETGlnLysArgHisAlaGl
                 81                            106
                  82
                 81

                        HaeIII
                          |
139 GTGGATGACCGAACACGGCCGTGTTTACGCAGATGCGAACGAGAAAAACAACCGCTACGCTGTTTTCAA  207
    uTrpMETThrGluHisGlyArgValTyrAlaAspAlaAsnGluLysAsnAsnArgTyrAlaValPheLy
                        157
```

Complete nucleotide sequence of B. campestris cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIGURE 4A

```
                                                  HpaII      DraI
                                                  |          |
208 ACGCAACGTGGAACGCATTGAACGCTTAAATGACGTTCAATCCGGACTAACGTTTAAACTCGCGGTGAA  276
    sArgAsnValGluArgIleGluArgLeuAsnAspValGlnSerGlyLeuThrPheLysLeuAlaValAs
                                                  250        263

        Sau3AI       EcoRI        RsaI
        |            |            |
277 CCAGTTTGCTGATCTAACCAACGAAGAATTCCGTTCTATGTACACTGGTTTCAAAGGAAACTCTGTGTT  345
    nGlnPheAlaAspLeuThrAsnGluGluPheArgSerMETTyrThrGlyPheLysGlyAsnSerValLe
        287          303          318

                                RsaI
       TaqI                      KpnI                 HpaII
       |                        | |                   |
346 GTCTAGTCGAACTAAACCAACGTCGTTTAGGTACCAAAACGTTTCTTCTGATGCGTTGCCGGTTTCTGT  414
    uSerSerArgThrLysProThrSerPheArgTyrGlnAsnValSerSerAspAlaLeuProValSerVa
       353                        380                 405
                                378

                AluI          Sau3AI       Sau3AI
                |             |            |
415 TGATTGGAGGAAGAAAGGAGCTGTGACTCCTATCAAGGATCAAGGCTTATGCGGATCTTGTTGGGCGTT  483
    lAspTrpArgLysLysGlyAlaValThrProIleLysAspGlnGlyLeuCysGlySerCysTrpAlaPh
                435           452          468
```

FIGURE 4B

```
      PvuII
      AluI
      |
484 TTCAGCTGTTGCGGCTATAGAAGGAGTAGCACAGATAAAGAAAGGGAAACTCATTTCTTTGTCTGAACA 552
    eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysLysGlyLysLeuIleSerLeuSerGluGl
          489
          489

                TaqI
             SalI
                HincII
             AluI AccI
             |   |||
553 AGAGCTTGTCGACTGCGACACAAACGATGGTGGCTGCATGGGCGGTTTGATGGATACAGCGTTTAACTA 621
    nGluLeuValAspCysAspThrAsnAspGlyGlyCysMETGlyGlyLeuMETAspThrAlaPheAsnTy
          557   562
                560
                561
                562

622 CACAATAACTATTGGCGGCTTAACCTCTGAATCAAATTATCCTTATAAAAGCACAAACGGCACTTGCAA 690
    rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyrProTyrLysSerThrAsnGlyThrCysAs

                      HpaII
                      |
691 CTTCAATAAAACTAAACAGATAGCAACTTCTATCAAAGGTTTTGAGGATGTCCCGGCTAACGATGAGAA 759
    nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyPheGluAspValProAlaAsnAspGluLy
                            744
```

FIGURE 4C

```
                                  HpaII
                                  |
760 AGCCCTAATGAAGGCAGTGGCACACCACCCGGTTAGCATTGGAATAGCGGAGGAGATATTGGTTTCCA  828
    sAlaLeuMETLysAlaValAlaHisHisProValSerIleGlyIleAlaGlyGlyAspIleGlyPheGl
                                  789

                                                     Sau3AI
                HpaII                                BclI
                |                                    |
829 ATTCTATTCGTCCGGTGTGTTCAGCGGAGAATGCACAACTCATCTTGATCACGGGGTAACTGCGGTTGG  897
    nPheTyrSerSerGlyValPheSerGlyGluCysThrThrHisLeuAspHisGlyValThrAlaValGl
                841                                  875
                                                     875

                                  ScaI
                                      Sau3AI
       Sau3AI                     RsaI
     HaeIII                           BamHI      EcoRI     AvaII
     |  |                         |   |          |         |
898 ATACGGCCGATCTAAAAACGGATTAAAGTACTGGATCCTCAAGAATTCATGGGGACCAAAATGGGGAGA  966
    yTyrGlyArgSerLysAsnGlyLeuLysTyrTrpIleLeuLysAsnSerTrpGlyProLysTrpGlyGl
     904                                  931        941       951
       906                        927
                                      931
                                  927

               Sau3AI        EcoRV
               |             |
967 ACGTGGATACATGAGGATCAAAAAAGATATCAAGCCTAAACACGGACAATGTGGTCTTGCCATGAATGC 1035
    uArgGlyTyrMETArgIleLysLysAspIleLysProLysHisGlyGlnCysGlyLeuAlaMETAsnAl
               982           995
```

FIGURE 4D

```
                                                         HindIII
      RsaI                                           HpaII   AluI
        |                                              |    |  |
1036 TTCGTACCCAACTATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAATAAATGTGTGTGTTGG 1104
     aSerTyrProThrMET
         1041                                        1073     1081
                                                           1079

1105 TTATAATTTAAGACTCTGTTGCATGTAATTTGTGAAATGGTAAGTTTATGTGATGCAAAAGATTTGATA 1173

1174 AAAAAAAAAAAAA 1186
```

FIGURE 4E

```
3H11  TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA  51

3H11  GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102

3H11  CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153

3H11  TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204
                                    TGCTCATCAATTAGCAATTAATCC

3H11  AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255
2A11  AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC
            METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe

3H11  GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTCGAAAATG 306
2A11  GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTTCGAAAATG
      ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET

3H11  CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357
2A11  CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
      GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET

3H11  AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408
2A11  AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA
      LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer

3H11  AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459
2A11  AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG
      AsnSerAspCysIleGlyIleThrLeuCysGlnPhyCysLysGluLysThr

3H11  GACCAGTATGGTTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11  GACCAGTATGGTTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
      AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro

3H11  TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561
2A11  TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA

3H11  TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11  TAGTGTTGTCTGTACCTTTGGTGTGAAGAATGTGAATAAAGGGATACATAT

3H11  ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663
2A11  ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT

3H11  GATTGTTTGAATAAAAACATACCATGAGTGAAATAATTATTCCACATTAAT 714
2A11  GATTGTTTGAATAAAAACATACCATGAGTGAAATAATTATTCC

3H11  TCACGTATTTATTTCACTTATGATACGTATTTTTGTTCCTTTCGCGTAAAA 765
3H11  AAAAAAAAA  774
```

FIGURE 5

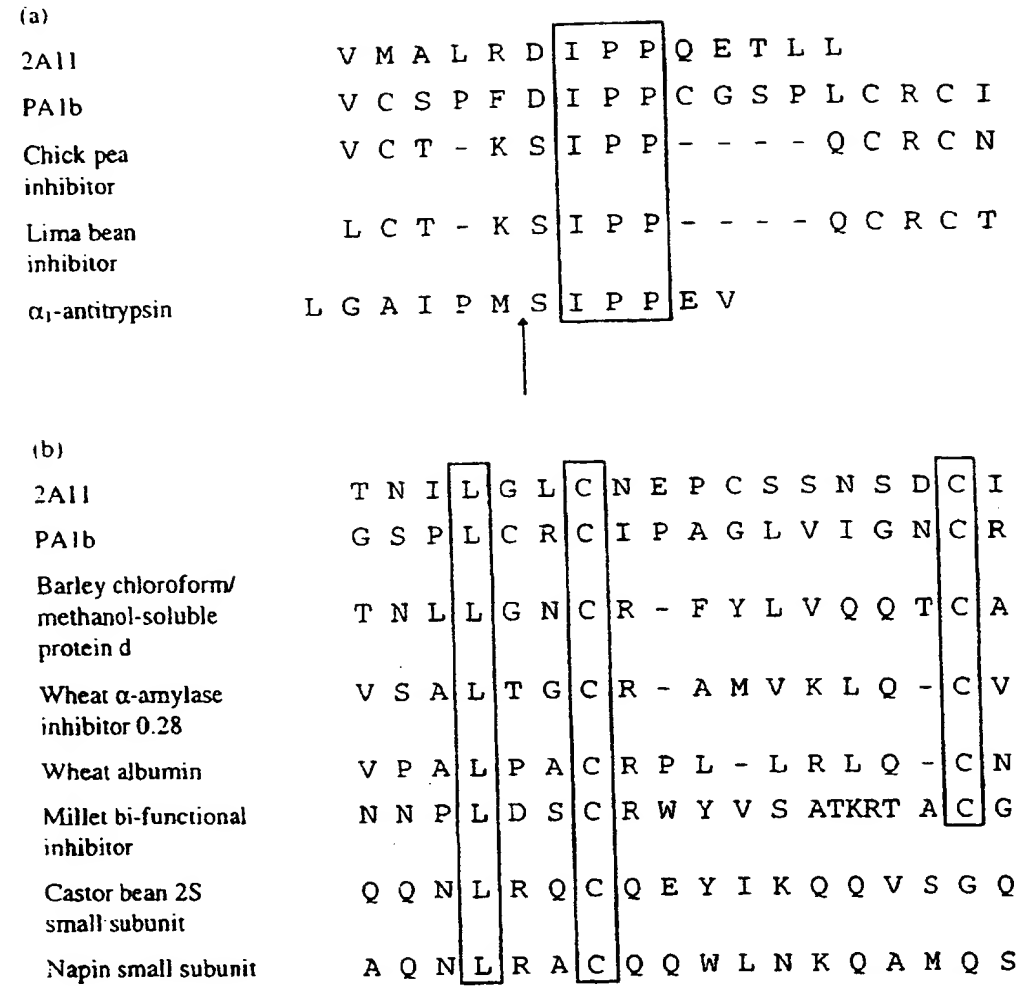


FIGURE 6

2A11 GENOMIC

```
CTCGAGCCCT TTAAAAAGTA TAGTCAATAT TTACGGTGAC CGTGAATTTC TTAATTATGA   60
TATATAATTT AAAAGAAATC ATGATCACAT TCTACTGATG AGAACATGTG CTAATCAAGG  120
GAAACATGG ATGTGAAAAA TACTTTTTGT TAAAAGTAAA AAAAAATGTG AAATTTTGTT  180
AGTTATTTAC TACCTATACA TTATTTGAGC ATGTGCAAAC TTTACAAATA CCTAATAGAA  240
GATTTTCACC TGCCTGTATA TATGTAAATT AATTATAATG AACACTCTCA CATAAAATAA  300
TTATCAGTAT ATACATTAAT ACTTGCCCTC CACAATGAAT TAAATAAAAT GTAGAACATG  360
ATCTACACTT CAATAAAACT AAGACCATAA AGAATAATTT CAAAATATAC ACATGTCAAC  420
AATAAATTAT TTGCATATTA TATTAACTTA CTAAACAATC TTTACTTTTG AAATATAAAA  480
ATAATCAAGT TATAAGTCTG CTCAAAGTAA AGCACTTGTT AGACTCATCT GATTTTGAGA  540
AGGTAAGCAA ATTGATGGTG CATAATAGTC ACAAGTAAAA TATAAAATAG ATTTCATTAG  600
TAAAATTGTT TTTTACTTTC TTTATATATA ATTATCAATA TCCTTCAATG GTAGGTTAAT  660
TATATTGTTA ACTTCTTGTT GAATTAAAGC AATAAGACAA GAATATTAAA GATAAAAGAA  720
CAATAAAAAT AGAAAGACTA AGAGATAAGA GTTTTCTTAT TCTTCTTTCA ATAAGTATCA  780
TCAAGTGTAT ACAATATAAA TTTTTGTATT TTTGATCTAT CTATTTATAA TGTTATATAT  840
AAGCATACAA AAGATCAGTC ATAAATATGA CTTTAATCAT GAAAATAATG AAAGAGATTA  900
```

FIGURE 7A

```
TGAAGGCGTA AGGTTACTAG AATAATAGTC ATTAAAAAAA GGGGTTATCT TTATAATTGA   960

ATAATTGATG AAGTAATGGA GATAATTAGT GAGCATAAAT TTTTTTAAAA AAATGGACAT  1020

TTACACTATA ATATTTTATA ACACTTTCCC TTAAACATCT AGGTATAAAT AATGAGTCTT  1080

GTCAAAATCT TAGTAGGAAA AATTCTGTGA AATTTTTTTA GTGAAAACAA ATGATATAAA  1140

TATCTTGAAT ACTCATTATT TGTTGTCTCA TTAAAAATCT TATCTGACCT ATAAAATAAA  1200

TTATTTGCTC AACTCAAAAT AGTTTTTCAT TCTAAAATTA GTATAATTAT TAGTGAATAT  1260

TTAATTAACA TAATTGTATA CTAAGGGGCC TATAAATTGG ATTCTTCTCA AAGAAAAATA  1320

AAATCACCAC ACAACTTTCT TCTTCTGCTC ATCAATTAGC AATTAATCCA AAACCATT    1378

ATG GCT GCC AAA AAT TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT     1426
MET Ala Ala Lys Asn Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val

CTT TTG ACG ACC ACT TTA GGTTCACAAC ACTTCTCCCT TATTTTGTTT           1474
Leu Leu Thr Thr Thr Leu

TCTTAATTTC TTGGAAGTCA TATGCATGTG TTTGGTATCA TGGTATATAT ATAAAGGAAA  1534

ATATTTTTCT TAATTACTGG TTTTCTAATG TTTGGTAGGT AATCGGAAAT TATTATGAGA  1594

TAATGAACTT GCAAAGTCAT TATTATATAA CTTTTTTTTT ATACTTTGAT TTAAGAATTC  1654

ATTTTTCTCA TTTTATATAA ACTTATTTTT CAACAGAAAA TATTTTTCGA ACTATTCAAA  1714

CACACCCTAA GACATTACAT ATATATATAT ATACACCCTC CGTTTTATAT TACTTAATGC  1774
```

FIGURE 7B

```
CTATTGAGTT GGCCCACCCT TTAAGAATGA TTCAATTAGA GATATGTTTT ACTAAATTAA  1834

CCTATGCTTT AAGACTCTAA ATTTGGCTAT TACTATTTTA CGTTGTAATT TAATGACAAA  1894

CATTTCATAA TGACTATAGT CTGAACTTAA TTAGACAGAC GTATCTATAG TTTGCTTACT  1954

AATGATTCAT AGCTATATAT TTGGAGAGGA GAGAGACAAA CGATATTAAG AAAGGGAGGA  2014

GAGAGGCGAG GTAAATCTGA AATAGAGAAG AGAAAGGCAA CCAATTTTGA TCATCTATCA  2074

TACTTTTGAT TATTATTTTT ATTATATGTA CGTTTACATT ACAGTTTTCG AATTCTTACA  2134

TTAATCTTAA TCATAATATA TACA GTT GAT ATG TCT GGA ATT TCG AAA ATG CAA  2188
                          Val Asp MET Ser Gly Ile Ser Lys MET Gln

GTG ATG GCT CTT CGA GAC ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG    2236
Val MET Ala Leu Arg Asp Ile Pro Pro Gln Glu Thr Leu Leu Lys MET

AAG CTA CTT CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC    2284
Lys Leu Leu Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser

TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT TGT AAG GAG    2332
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe Cys Lys Glu

AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT ACA TGC AAC CTG TTG CCT    2390
Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg Thr Cys Asn Leu Leu Pro

TGA ACAATATCAA TGATCTATCG ATCGATCTAT CTATCTATTT ATCTGTCTCT          2433

GCGCGTATAG TGTTGTCTGT ACCTTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT  2493

CTAGATATAT TCTAGGTAAT GTCCTATTGT ATTTAAAATT TGTAGCAATG ATTGTTTGAA  2553
```

FIGURE 7C

TAAAACATA	CCATGAGTGA	AATAATTATT	CCACATTAAT	TCACGTATTT	ATTTCACTTA	2613
TGATACGTAT	TTTGTTCCT	TTCGCGTAGA	TTTTTGATCC	TTTTCCCTTT	TGAATATTAA	2673
ACATTAAACA	CAAATAATGT	TTATTAAATT	AAGTTAATAT	TTTTATTTAG	CTATTTATAT	2733
TTTTATTTGA	AATCAAACTT	GATAAATATT	TATAAAGATA	ATTAACAAGT	AATGTGACAC	2793
TAACACCATG	TAATATTATC	TTGTCGTTAT	TTATGATAAT	ATTTTAAAAT	TATAATTTCA	2853
GTTAAAAAAT	TATTAAAAAA	ACATACTTTT	AAAAAGTGAG	TTAGCCTCCG	CTACCCACAT	2913
ACTTATGAAT	TGGACTAGTT	GTTTTTTGAC	CCACAAAAAG	AATGGGCTAA	TTAAACCTGA	2973
CCTATCAAAT	TTCAGAATCT	GCATAGATTA	GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	3033
ACAAAATATC	AACAAGGACG	TTATGTAAAG	ATGTTTAAGA	AGGAAAAAAG	ATTTCTAATA	3093
CATATGGACT	TTCAATATCC	CAACTTTGTC	TGGCGATCTG	AACCCTGCTT	AGTTTGTTGA	3153
TCATTAACTT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTTT	ATATGTTTAA	ACTTACAGAA	3213
AATACATATA	AATCTCTCAA	GACTTGGCAA	CATAATTTAC	TTTAGTACTT	AAACTACATG	3273
AAAATTTAAA	TATCCTTTTA	ACATCTTTGA	AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	3333
CACCTTGGAC	GTGGCCGGCA	CTCAAGAACC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	3393
GACTGACTAC	AAGCGGAAGG	CTAACTTAAG	TATACAAAAG	CTTAAAACTG	AATAAAATAA	3453
ACTTTACAAG	GTTTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT	TCAACTAGCC	3513

FIGURE 7D

ATAAAATAGA	CAACTTTAGT	CTTTAAAACA	TTTAATAAAA	TAAATGCAAA	ATATAGACTC	3573
CTTAACTAAA	CTGACTATCT	ATGGAGCCTC	TAATTGATAA	AGATGGAAGT	CGGGACAAGA	3633
CCACGACATC	CTGACTAAAC	TGAGAAGTAA	ATAAAATCCC	CCGGAAAAAA	AGGAGCCTCA	3693
CCATGGCTAA	CTCGAACTCG	GGGATATATC	AATGAAGCTC	CTGTTGATGA	TCTTGAAGAC	3753
ATGTCTCTGC	ATCATCAAAA	AGATGCAGGC	CAAATGGCTC	AGTACGTAAA	ATGTACGAGT	3813
ATGTAAGGGA	AATTCTAAAG	TATAACATAA	GCTTGATACT	TGAATAAAAG	GAAACATACT	3873
TACCTCTTTT	CAACTCAACT	CAAATTAAGA	ATAAGATACT	CAACTCAAAG	ATTAGGTATT	3933
CAACGCAAAT	ATGGCACTCT	ACTCAATGAA	GTACAAATTA	ACTCAGGATA	CTCGACTTAA	3993
GATACTCAAC	TCCCGACACT	CAACTGAACT	CATTTCAATA	TAAAGCAGCT	TAAAACAAGT	4053
TCAGTATAAA	GTAAAGTTGT	TTAAAAACAT	GATGTCAACT	CTGTGTGTAT	AATAAGGGAT	4113
ACAACATAAC	TTTGAAATGT	ATATAAAAAT	ACAATTAACT	GATGTATATA	AAAATACATT	4173
AATCTATGGG	AGATTCTCTA	ACCGACAACC	ATCACTTAAG	GGCTAAGATG	ATGATATAGC	4233
GATCTACCGC	ACGCTGCCAT	CGCATCTTAT	ACCCGGCCAA	AGGTATAAGA	CCTGAACTGC	4293
CTAATGAATC	CACTAATAAA	CTGTTAAAAG	GAATCATCTA	AAAAGTATGA	CCCTTTTCTA	4353
CCCATAGTGG	CTAACATGGT	TTATGGGGGC	TGTGAGTTAT	CTGAACTCTC	CCCCATATCG	4413

FIGURE 7E

GTGCTCAATA CTACTCCAAA AAATATACTG CTCTTATGTT TAAAAACATA CTGATTCTGT 4473

GGTTTGAAAT TATTGCTTAA AGCTTAGATT TTTGAAAAGC TCTCTTTTGA AAATCGTAGT 4533

TTCCTTTTTC TTCTATTAAA GCTAGACATA GGCTATGTAG AACTCTAGCT TACCTTCCTT 4593

CTCAAAAGTT TGAAAACATT TGCTTAGATT CTTAGGGACT ACTTAGTTCC CTTGTTGGAA 4653

TTC 4656

FIGURE 7F

PG GENOMIC

```
        10          20          30          40          50          60
                                                                      *
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT ATAACAGTGG

        70          80          90         100         110         120
                                                                      *
TAAAGCACCT TAAGAAACCA TAGTTTGAAA GGTTACCAAT GCGCTATATA TTAATCAACT

       130         140         150         160         170         180
                                                                      *
TGATAATATA AAAAAAATTT CAATTCGAAA AGGGCCTAAA ATATTCTCAA AGTATTCGAA

       190         200         210         220         230         240
                                                                      *
ATGGTACAAA ACTACCATCC GTCCACCTAT TGACTCCAAA ATAAAATTAT TATCCACCTT

       250         260         270         280         290         300
                                                                      *
TGAGTTTAAA ATTGACTACT TATATAACAA TTCTAAATTT AAACTATTTT AATACTTTTA

       310         320         330         340         350         360
                                                                      *
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTTA TGAATATCAT TTATAAACCA

       370         380         390         400         410         420
                                                                      *
ACCAACTACC AACTCATTAA TCATTAAATC CCACCCAAAT TCTACTATCA AAATTGTCCT

       430         440         450         460         470         480
                                                                      *
AAACACTACT AAAACAAGAC GAAATTGTTC GAGTCCGAAT CGAAGCACCA ATCTAATTTA

       490         500         510         520         530         540
                                                                      *
GGTTGAGCCG CATATTTAGG AGGACACTTT CAATAGTATT TTTTTCAAGC ATGAATTTGA
       550         560         570         580         590         600
                                                                      *
AATTTAAGAT TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCATGCC TTTTTTAAAT

       610         620         630         640         650         660
                                                                      *
ATAATTATAT AAATATTTAT GATTTGTTTT AAATATTAAA ACTTGAATAT ATTATTTTTT

       670         680         690         700         710         720
                                                                      *
TAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA AGGAATAATT AAGATGAACA
       730         740         750         760         770         780
                                                                      *
TAGTGTTTAA TTAGTAATGG ATGGGTAGTA AATTTATTTA TAAATTATAT CAATAAGTTA

       790         800         810         820         830         840
                                                                      *
AATTATAACA AATATTTGAG CGCCATGTAT TTTAAAAAAT ATTAAATAGT TTGAATTTAA
```

FIGURE 8A

```
      850         860         870         880         890         900
                                                                    *
AACCGTTAGA TAAATGGTCA ATTTTGAACC CAAAAGTGGA TGAGAAGGGT ATTTTAGAGC

      910         920         930         940         950         960
                                                                    *
CAATAGGRGG ATGAGAAGGA TATTTTGAAG CCAATATGTG ATGGATGAAG GATAATTTTG

      970         980         990        1000        1010        1020
                                                                    *
TATCATTTCT AATACTTTAA AGATATTTTA GGTCATTTTC CCTTCTTTAG TTTATAGACT

     1030        1040        1050        1060        1070        1080
                                                                    *
ATAGTGTTAG TTCATCGAAT ATCATCTATT ATTTCCGTCT TAAATTATTT TTTATTTTAT

     1090        1100        1110        1120        1130        1140
                                                                    *
AAATTTTTTA AAAATAAATT ATTTTTTCCA TTTAACTTTG ATTGTAATTA ATTTTTAAAA

     1150        1160        1170        1180        1190        1200
                                                                    *
ATTACCAACA TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTTA

     1210        1220        1230        1240        1250        1260
                                                                    *
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA AAAATTGAGA

     1270        1280        1290        1300        1310        1320
                                                                    *
CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAAACTCT TTCGTCTAAA TATCTCTCAT

     1330        1340        1350        1360        1370        1380
                                                                    *
CCAAACTAAT ATAATACCCA TTATAATTAA CCATATTGAC CAACTCAAAC CCCTTAAAAT

     1390        1400        1410        1420        1430        1440
                                                                    *
CTATAAATAG ACAAACCCTT CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTTCA

     1450        1460        1470        1480        1490        1500
                                                                    *
ATAGACAAGT TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT

     1510        1520        1530        1540        1550        1560
                                                                    *
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCAA CTTGTAGAAG CAATGTTATT

     1570        1580        1590        1600        1610        1620
                                                                    *
GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG AACAAGAATT TGCTCATGAT

     1630        1640        1650        1660        1670        1680
                                                                    *
TTTCAAGCTT ATCTTTCTTA TTTGAGCAAA AATATTGAAA GCAACAATAA TATTGACAAG
```

FIGURE 8B

```
      1690        1700        1710        1720        1730        1740
                                                              *
GTTGATAAAA ATGGGATTAA AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA

      1750        1760        1770        1780        1790        1800
                                                              *
AAAACATATG ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAT

      1810        1820        1830        1840        1850        1860
                                                              *
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA AGTAGAAAAT

      1870        1880        1890        1900        1910        1920
                                                              *
TATTTTCTCG TTTTTAGTAA TTAAAGGTGA AAAATGAGTT TTCTCGTAAG CGAGGAAAGT

      1930        1940        1950        1960        1970        1980
                                                              *
CATTTTCCAT GGAACTGTAT TTTTTTTTTA CTTTTAATAA CGTCATAGTA TTTGCTATAC

      1990        2000        2010        2020        2030        2040
                                                              *
TCAAGAATAA GACACTATTA TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG

      2050        2060        2070        2080        2090        2100
                                                              *
CTAATATAAC TATCAATTTC TTATATGTAT ATTTTTCAAC CAAAATAACA AAGCGTAATC

      2110        2120        2130        2140        2150        2160
                                                              *
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT TATTTAATTT

      2170        2180        2190        2200
TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT CGAATTC
```

FIGURE 8C

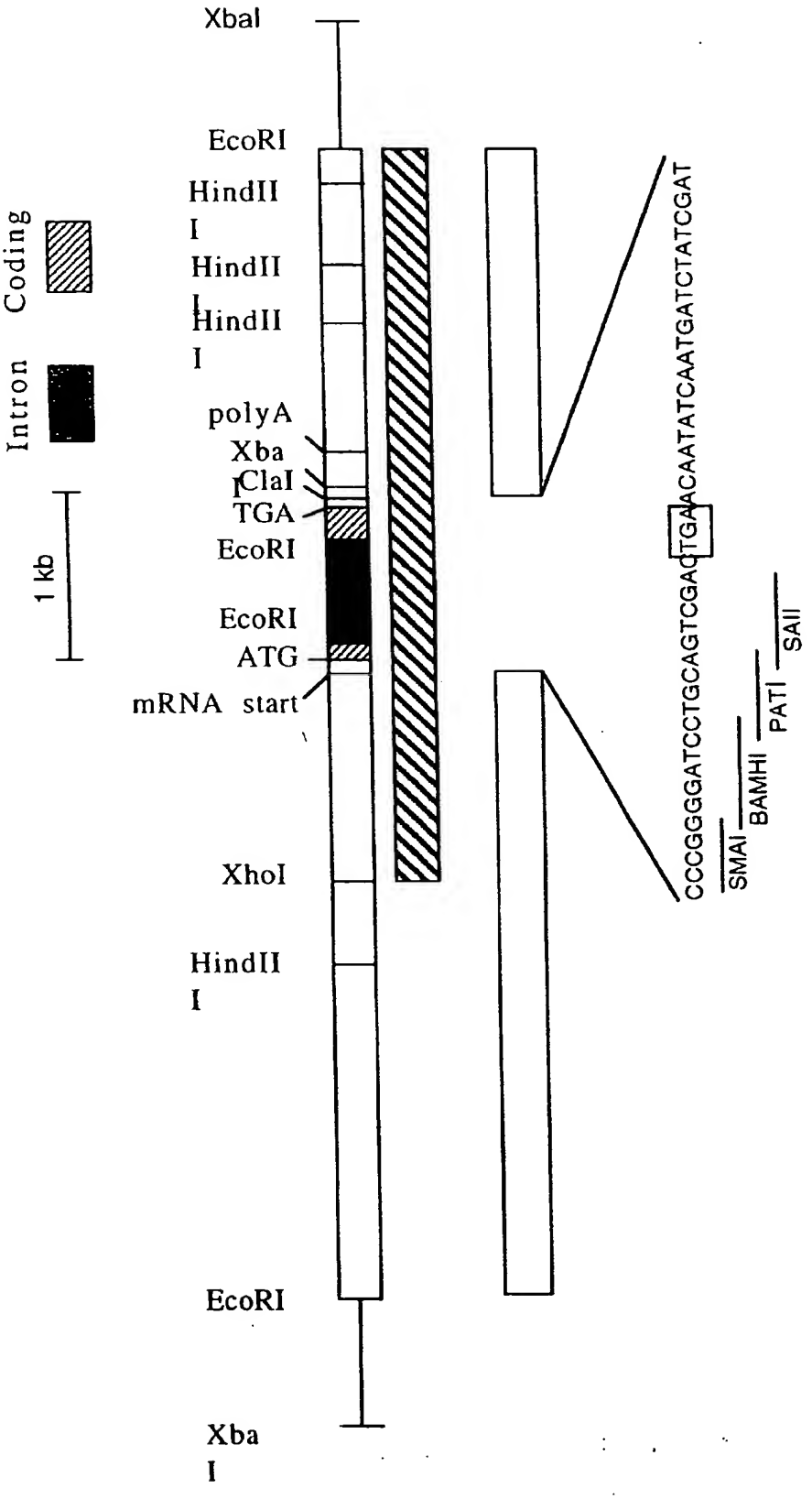
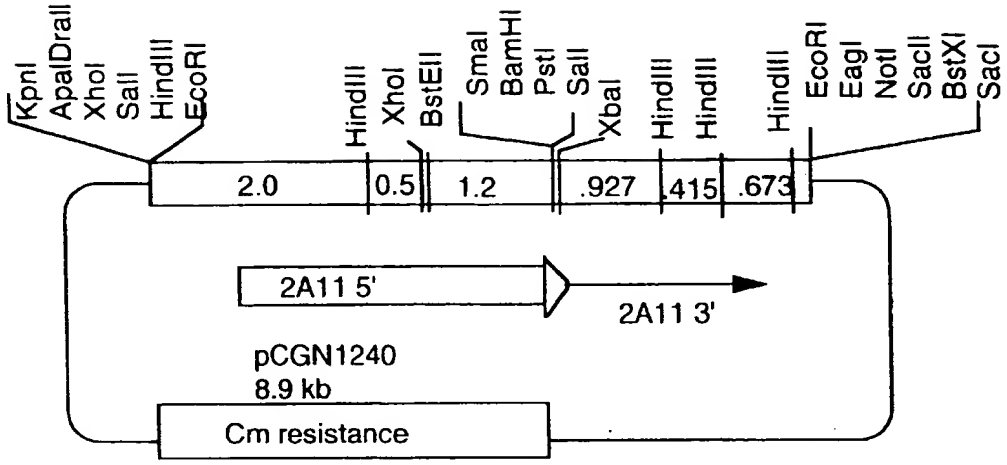


FIGURE 9



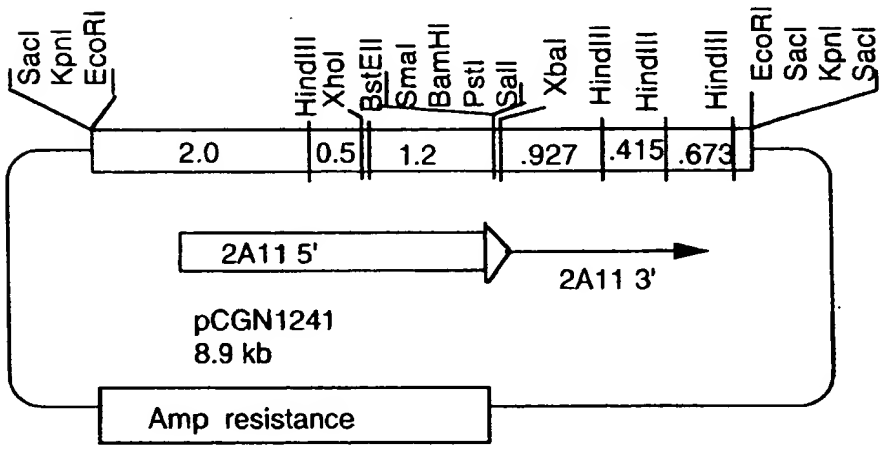
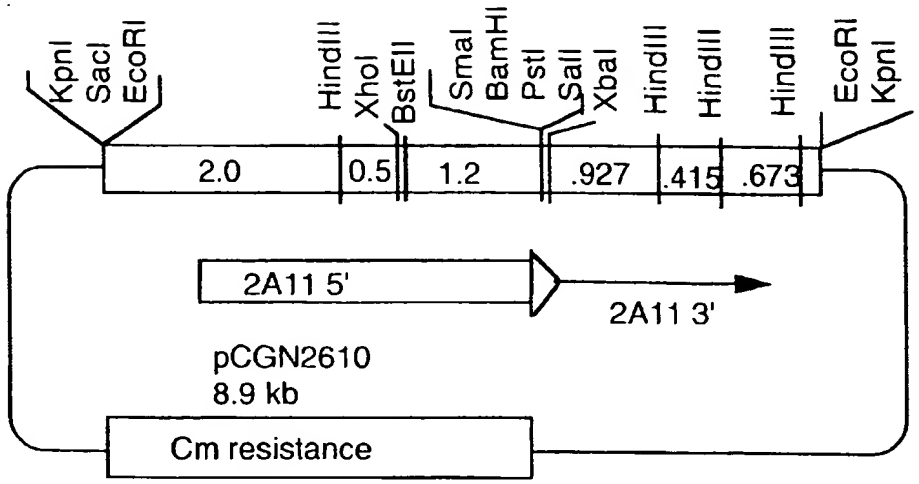


FIGURE 10A



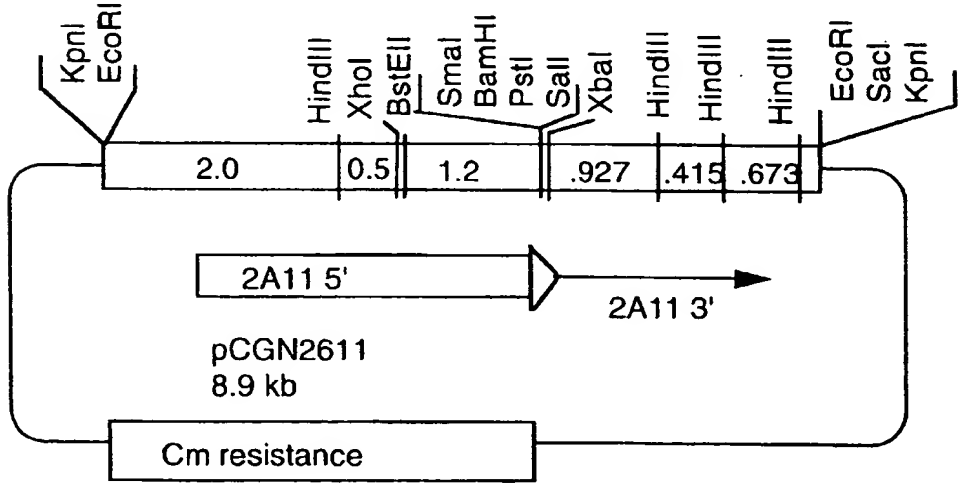


FIGURE 10B